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Laboratory of Molecular Medicine, University of Tokyo.

We examined loss of heterozygosity (LOH) in 37 esophageal squamous cell carcinomas using microsatellite markers mapped to 9q31-34.1. Partial or interstitial deletions were detected in 13 of them and the detailed deletion map defined a commonly deleted region between the D9S262 and D9S154 loci at 9q31-q32. The genetic distance was estimated to be approximately 4 cM. To narrowly define the commonly deleted region, we analyzed six microsatellite markers from YAC (yeast artificial chromosome) clones covering the deleted region. As the distal 9q region also has been implicated as the site of a tumor suppressor gene(s) related to squamous cell carcinomas of other tissues, our results provide useful information for attempts to identify a common gene for carcinoma of this cell type.

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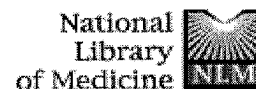
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PMID: 8920661 [PubMed - indexed for MEDLINE]

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63110, USA.

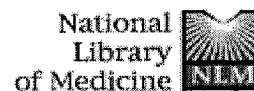
In this study we exploit the unique genetic resource of inbred mouse major histocompatibility complex (H2) congenic and recombinant strains to const resolution map of microsatellite loci in and around the H2 region, as well as independent genetic map of other loci on mouse Chromosome (Chr) 17. Mi loci were analyzed in 11 C57BL/10 (B10) strains to determine the size of th interval in each. The length of the congenic interval found in each strain vai Interestingly, the intervals were generally smaller than statistical expectatio: the observed congenic intervals were still sufficiently long that these strains wild-derived H2 congenics are an important source of genetic variability. T ends of the various congenic intervals and the recombinants were used to cc map. This map will be useful for physical cloning and to help localize nove evidence of the mapping application of congenic strains, locational informa derived about Trp53-ps and Stl.

PMID: 8535063 [PubMed - indexed for MEDLINE]

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[PubMed Central](#)[Privacy Policy](#)☐ 1: Genomics 1995 Aug 10;28(3):566-569[Related Articles, OMIM](#)**Genetic association between chromosome 8 microsatellite (MS8) and Werner syndrome (WRN): chromosome microdissection and homozygosity mapping.****Ye L, Nakura J, Mitsuda N, Fujioka Y, Kamino K, Ohta T, Jinno Y, Nishimura Miki T, Ogihara T.**

Department of Geriatric Medicine, Osaka University Medical School, Japan

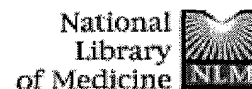
Werner syndrome (WRN) is an autosomal recessive disorder characterized by premature aging that has been mapped to the short arm of chromosome 8, 8p11.2-p12. In a genetic map around the WRN region, we have isolated eight microsatellites in the region from a microdissection library. We typed members of Japanese families with WRN on the basis of homozygosity mapping analysis. There was no obligate recombination between the WRN locus and microsatellite clone, MS8-134. The maximum lod score was 20.28 at $\theta = 0.00$. Alleles for MS8-134 showed a strong association with WRN in a case-control study (OR = 3.55, 95% CI 1.56-8.0). Such microsatellites from a microdissection library of the definite chromosome 8 may be useful for positional cloning of the WRN gene.

PMID: 7490095 [PubMed - indexed for MEDLINE]

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☐ 1: Genomics 1996 Mar 15;32(3):458-461

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**Physical mapping of 49 microsatellite markers on chromosome correlation with the genetic linkage map.****Reguigne-Arnould I, Faure S, Chery M, Mota-Viera L, Mollicone R, C Oriol R, Couillin P.**

INSERM U178, Villejuif, France. arnould@infobiogen.fr

We have regionally localized 49 microsatellite markers developed by Genet panel of previously characterized somatic cell hybrids that retain fragments chromosome 19. The tight correlation observed between the physical and the orders of the microsatellites provide cytogenetic anchorages to the genetic map. We propose a position for the centromere just above D19S415, from the study of hybrids, each of which retains one of the two derivatives of a balanced translocation (1;19)(q11;q11). Microsatellites, which can be identified by a standard PCR, are useful tools for the localization of disease genes and for the establishment of cosmid contigs. These markers can also judiciously be used for the characterization of new hybrid cell line panels. We report such a characterization of 11 clones, which were obtained by irradiation-fusion. Using the whole hybrid panel, we were able to define the order of 12 pairs of genetically colocalized microsatellites. As expected, gene mapping by the combined use of microsatellites and hybrid cell lines, we assigned the PVS locus between the 19q13.2 markers D19S417 and D19S415, which confirmed the locations of fucosyltransferase loci FUT1, FUT2, and FUT5.

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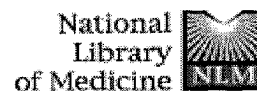
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☐ 1: Chromosome Res 1999;7(8):635-640

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Differentiation of Z and W chromosomes revealed by replication and FISH mapping of sex-chromosome-linked DNA markers in cassowary (Aves, Ratitae).**Nishida-Umehara C, Fujiwara A, Ogawa A, Mizuno S, Abe S, Yoshida**

Chromosome Research Unit, Faculty of Science, Hokkaido University, Sap

We identified sex chromosomes of the double-wattled cassowary (*Casuariu* by a replication banding method. The acrocentric Z chromosome, the fifth l males and slightly smaller W chromosome show no sign of heterochromatin share a nearly identical banding pattern in the distal half of the long arm. Th chromosomes were further characterized by FISH with three probes linked W chromosome in most avian species examined thus far. Contrary to the sit chicken, we obtained positive signals with Z-specific ZOV3 and W-specific the distal region of both Z and W chromosomes. However, IREBP signals l the proximal half of the Z chromosome were not detected on the W chromo structural rearrangements such as deletions and inversions might have been step of W chromosome differentiation from an ancestral homomorphic pair species.

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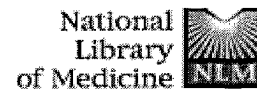
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☐ 1: Genomics 1998 Apr 15;49(2):265-274

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**A comprehensive microsatellite linkage map of the chicken genome****Groenen MA, Crooijmans RP, Veenendaal A, Cheng HH, Siwek M, van der Poel JJ.**

Department of Animal Breeding, Wageningen Institute of Animal Sciences, Agricultural University, The Netherlands. martien.groenen@alg.vf.wau.nl

A comprehensive linkage map of the chicken genome has been developed by analysis of 430 microsatellite markers within a cross between two extreme lines. The population used to construct the linkage map consists of 10 families with 458 F2 individuals. The number of informative meioses per marker varied from 900 with an average of 400. The markers were placed into 27 autosomal linkage groups and a Z-chromosome-specific linkage group. In addition, 6 markers were unique to which was Z chromosome specific. The coverage within linkage groups is 3. Although, as in other species, the genetic map of the heterogametic sex (female) is shorter than the genetic map of the homogametic sex (male), the overall difference in length is small (1.15%). Forty-five of the markers represent identified genes. Database homology searches with the anonymous markers resulted in the identification of a further 9 genes, bringing the total number of genes/ESTs on the current map to 54. The mapping of these genes led to the identification of two new regions of conserved synteny between human and chicken and confirmed other previously identified regions of conserved synteny between human and chicken. The linkage map has 210 cM common with the linkage maps based on the East Lansing and Compton reference populations, and most of the corresponding linkage groups in the different maps readily aligned.

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